

OIPE

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/10/014,896

DATE: 01/02/2002  
 TIME: 14:47:27

Input Set : A:\LEX-0280-USA SEQLIST.txt  
 Output Set: N:\CRF3\01022002\J014896.raw

ENTERED

4 <110> APPLICANT: Yu, Xuanchuan  
 5 Miranda, Maricar  
 6 Friddle, Carl Johan  
 8 <120> TITLE OF INVENTION: Novel Human Proteases and  
 9 Polynucleotides Encoding the Same  
 11 <130> FILE REFERENCE: LEX-0280-USA  
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/014,896  
 C--> 13 <141> CURRENT FILING DATE: 2001-12-11  
 13 <150> PRIOR APPLICATION NUMBER: US 60/255,567  
 14 <151> PRIOR FILING DATE: 2000-12-14  
 16 <160> NUMBER OF SEQ ID NOS: 4  
 18 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
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 21 <211> LENGTH: 1509  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Homo sapiens  
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 27 accgtctcca gatcgatggg cccgaggagc ggggagcatc aaagggcgtc gcgaatccct 120  
 28 tctcagttca gcaaagagga acgcgtcgcg atgaaagagg cgctgaaagg tgccatccag 180  
 29 attccaacag tgacttttag ctctgagaag tccaatacta cagccctggc tgagtccgga 240  
 30 aaatacattc ataaagtctt tcctacagtg gtcagacca gctttatcca gcatgaagtc 300  
 31 gtggaagagt atagccacct gttcactatc caaggctcgg accccagctt gcagccctac 360  
 32 ctgctgatgg ctcactttga tgtggtgcct gccctgaag aaggctggga ggtgccccca 420  
 33 ttctctgggt tggagcgtga tggcgtcatc tatggtcggg gcacactgga cgacaagaac 480  
 34 tctgtgatgg cattactgca ggccttggag ctctgctga tcaggaagta catccccga 540  
 35 agatctttct tcattttctt gggccatgat gaggagtcac cagggaacagg ggctcagagg 600  
 36 atctcagccc tgctacagtc aaggggcgtc cagctagcct tcattgtgga cgaggggggc 660  
 37 ttcatcttgg atgatttcat tcctaacttc aagaagccca tcgccttgat tgcagtctca 720  
 38 gagaaggggt ccatgaacct catgctgcaa gtaaacaatga cttcaggcca ctcttcagct 780  
 39 cctccaaagg agacaagcat tggcatcctt gcagctgctg tcagccgatt ggagcagaca 840  
 40 ccaatgccta tcatatttgg aagcgggaca gtggtgactg tattgcagca actggcaaat 900  
 41 gagtttccct tccctgtcaa tataatcctg agcaacccat ggctatttga accacttata 960  
 42 agcagggtta tggagagaaa tcccttaacc aatgcaataa tcaggaccac cacggcactc 1020  
 43 accatattca aagcaggggt caagttcaat gtcatcccc cagtggcca ggccacagtc 1080  
 44 aacttccgga ttcaccctgg acagacagtc caagaggtcc tagaactcac gaagaacatt 1140  
 45 gtggctgata acagagtcca gttccatgtg ttgagtgcct ttgacccct ccccgctcagc 1200  
 46 ccttctgatg acaaggcctt gggtaccag ctgctcgcgc agaccgtaca gtccgtcttc 1260  
 47 ccggaagtca atattactgc ccagttact tctattggca acacagacag ccgattcttt 1320  
 48 acaaacctca ccattggcat ctacaggttc taccctatct acatacagcc tgaagacttc 1380  
 49 aaacgcatcc atggagtcaa cgagaaaatc tcagtccaag cctatgagac ccaagtga 1440  
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 53 <210> SEQ ID NO: 2  
 54 <211> LENGTH: 502  
 55 <212> TYPE: PRT  
 56 <213> ORGANISM: Homo sapiens

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58 &lt;400&gt; SEQUENCE: 2

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59 Met Ala Gln Arg Cys Val Cys Val Leu Ala Leu Val Ala Met Leu Leu
60 1 5 10 15
61 Leu Val Phe Pro Thr Val Ser Arg Ser Met Gly Pro Arg Ser Gly Glu
62 20 25 30
63 His Gln Arg Ala Ser Arg Ile Pro Ser Gln Phe Ser Lys Glu Glu Arg
64 35 40 45
65 Val Ala Met Lys Glu Ala Leu Lys Gly Ala Ile Gln Ile Pro Thr Val
66 50 55 60
67 Thr Phe Ser Ser Glu Lys Ser Asn Thr Thr Ala Leu Ala Glu Phe Gly
68 65 70 75 80
69 Lys Tyr Ile His Lys Val Phe Pro Thr Val Val Ser Thr Ser Phe Ile
70 85 90 95
71 Gln His Glu Val Val Glu Glu Tyr Ser His Leu Phe Thr Ile Gln Gly
72 100 105 110
73 Ser Asp Pro Ser Leu Gln Pro Tyr Leu Leu Met Ala His Phe Asp Val
74 115 120 125
75 Val Pro Ala Pro Glu Glu Gly Trp Glu Val Pro Pro Phe Ser Gly Leu
76 130 135 140
77 Glu Arg Asp Gly Val Ile Tyr Gly Arg Gly Thr Leu Asp Asp Lys Asn
78 145 150 155 160
79 Ser Val Met Ala Leu Leu Gln Ala Leu Glu Leu Leu Ile Arg Lys
80 165 170 175
81 Tyr Ile Pro Arg Arg Ser Phe Phe Ile Ser Leu Gly His Asp Glu Glu
82 180 185 190
83 Ser Ser Gly Thr Gly Ala Gln Arg Ile Ser Ala Leu Leu Gln Ser Arg
84 195 200 205
85 Gly Val Gln Leu Ala Phe Ile Val Asp Glu Gly Gly Phe Ile Leu Asp
86 210 215 220
87 Asp Phe Ile Pro Asn Phe Lys Lys Pro Ile Ala Leu Ile Ala Val Ser
88 225 230 235 240
89 Glu Lys Gly Ser Met Asn Leu Met Leu Gln Val Asn Met Thr Ser Gly
90 245 250 255
91 His Ser Ser Ala Pro Pro Lys Glu Thr Ser Ile Gly Ile Leu Ala Ala
92 260 265 270
93 Ala Val Ser Arg Leu Glu Gln Thr Pro Met Pro Ile Ile Phe Gly Ser
94 275 280 285
95 Gly Thr Val Val Thr Val Leu Gln Gln Leu Ala Asn Glu Phe Pro Phe
96 290 295 300
97 Pro Val Asn Ile Ile Leu Ser Asn Pro Trp Leu Phe Glu Pro Leu Ile
98 305 310 315 320
99 Ser Arg Phe Met Glu Arg Asn Pro Leu Thr Asn Ala Ile Ile Arg Thr
100 325 330 335
101 Thr Thr Ala Leu Thr Ile Phe Lys Ala Gly Val Lys Phe Asn Val Ile
102 340 345 350
103 Pro Pro Val Ala Gln Ala Thr Val Asn Phe Arg Ile His Pro Gly Gln
104 355 360 365
105 Thr Val Gln Glu Val Leu Glu Leu Thr Lys Asn Ile Val Ala Asp Asn
106 370 375 380

```

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107 Arg Val Gln Phe His Val Leu Ser Ala Phe Asp Pro Leu Pro Val Ser
108 385 390 395 400
109 Pro Ser Asp Asp Lys Ala Leu Gly Tyr Gln Leu Leu Arg Gln Thr Val
110 405 410 415
111 Gln Ser Val Phe Pro Glu Val Asn Ile Thr Ala Pro Val Thr Ser Ile
112 420 425 430
113 Gly Asn Thr Asp Ser Arg Phe Phe Thr Asn Leu Thr Thr Gly Ile Tyr
114 435 440 445
115 Arg Phe Tyr Pro Ile Tyr Ile Gln Pro Glu Asp Phe Lys Arg Ile His
116 450 455 460
117 Gly Val Asn Glu Lys Ile Ser Val Gln Ala Tyr Glu Thr Gln Val Lys
118 465 470 475 480
119 Phe Ile Phe Glu Leu Ile Gln Asn Ala Asp Thr Asp Gln Glu Pro Val
120 485 490 495
121 Ser His Leu His Lys Leu
122 500
124 <210> SEQ ID NO: 3
125 <211> LENGTH: 1086
126 <212> TYPE: DNA
127 <213> ORGANISM: Homo sapiens
129 <400> SEQUENCE: 3
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131 accgtctcca gatcgatggg cccgaggagc ggggagcatc aaagggcgtc gcgaatccct 120
132 tctcagttca gcaaagagga acgcgtcgcg atgaaagagg cgctgaaagg tgccatccag 180
133 attccaacag tgacttttag ctctgagaag tccaatacta cagccctggc tgagttcgga 240
134 aaatacatc ataaagtctt tcctacagt gtcagcacca gctttatcca gcatgaagtc 300
135 gtggaagagt atagccacct gtccactatc caaggctcgg accccagctt gcagccctac 360
136 ctgctgatgg ctacttttga tgtggtgcct gccctgaag aaggctggga ggtgccccca 420
137 tctcttggtg tggagcgtga tggcgtcatc tatggtcggg gcacactgga cgacaagaac 480
138 tctgtgatgg cattactgca ggccttgag ctctgtctga tcaggaagta catcccccca 540
139 agatctttct tcatttctct gggccatgat gaggagtcac caggacagg ggctcagagg 600
140 atctcagccc tgctacagtc aagggcgctc cagctagcct tcattgtgga cgaggggggc 660
141 ttcattcttg atgatttcat tcctaacttc aagaagccca tcgccttgat tgcagtctca 720
142 gagaagggtt ccatgaacct catgctgcaa gtaaacatga cttcaggcca ctcttcagct 780
143 cctccaaagg agacaagcat tggcatcctt gcagctgctg tcagccgatt ggagcagaca 840
144 ccaatgccta tcatatttgg aagcgggaca gtggtgactg tattgcagca actggcaaact 900
145 gaggtttatg gagagaaatc ccttaaccaa tgcaataatc aggaccacca cggcactcac 960
146 catattcaaa gcaggggtca agttcaatgt catcccccca gtggccagg ccacagtcaa 1020
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151 <211> LENGTH: 361
152 <212> TYPE: PRT
153 <213> ORGANISM: Homo sapiens
155 <400> SEQUENCE: 4
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157 1 5 10 15
158 Leu Val Phe Pro Thr Val Ser Arg Ser Met Gly Pro Arg Ser Gly Glu
159 20 25 30

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```

160 His Gln Arg Ala Ser Arg Ile Pro Ser Gln Phe Ser Lys Glu Glu Arg
161          35          40          45
162 Val Ala Met Lys Glu Ala Leu Lys Gly Ala Ile Gln Ile Pro Thr Val
163          50          55          60
164 Thr Phe Ser Ser Glu Lys Ser Asn Thr Thr Ala Leu Ala Glu Phe Gly
165 65          70          75          80
166 Lys Tyr Ile His Lys Val Phe Pro Thr Val Val Ser Thr Ser Phe Ile
167          85          90          95
168 Gln His Glu Val Val Glu Glu Tyr Ser His Leu Phe Thr Ile Gln Gly
169          100          105          110
170 Ser Asp Pro Ser Leu Gln Pro Tyr Leu Leu Met Ala His Phe Asp Val
171          115          120          125
172 Val Pro Ala Pro Glu Glu Gly Trp Glu Val Pro Pro Phe Ser Gly Leu
173          130          135          140
174 Glu Arg Asp Gly Val Ile Tyr Gly Arg Gly Thr Leu Asp Asp Lys Asn
175 145          150          155          160
176 Ser Val Met Ala Leu Leu Gln Ala Leu Glu Leu Leu Leu Ile Arg Lys
177          165          170          175
178 Tyr Ile Pro Arg Arg Ser Phe Phe Ile Ser Leu Gly His Asp Glu Glu
179          180          185          190
180 Ser Ser Gly Thr Gly Ala Gln Arg Ile Ser Ala Leu Leu Gln Ser Arg
181          195          200          205
182 Gly Val Gln Leu Ala Phe Ile Val Asp Glu Gly Gly Phe Ile Leu Asp
183          210          215          220
184 Asp Phe Ile Pro Asn Phe Lys Lys Pro Ile Ala Leu Ile Ala Val Ser
185 225          230          235          240
186 Glu Lys Gly Ser Met Asn Leu Met Leu Gln Val Asn Met Thr Ser Gly
187          245          250          255
188 His Ser Ser Ala Pro Pro Lys Glu Thr Ser Ile Gly Ile Leu Ala Ala
189          260          265          270
190 Ala Val Ser Arg Leu Glu Gln Thr Pro Met Pro Ile Ile Phe Gly Ser
191          275          280          285
192 Gly Thr Val Val Thr Val Leu Gln Gln Leu Ala Asn Glu Val Tyr Gly
193          290          295          300
194 Glu Lys Ser Leu Asn Gln Cys Asn Asn Gln Asp His His Gly Thr His
195 305          310          315          320
196 His Ile Gln Ser Arg Gly Gln Val Gln Cys His Pro Pro Ser Gly Pro
197          325          330          335
198 Gly His Ser Gln Leu Pro Asp Ser Pro Trp Thr Asp Ser Pro Arg Gly
199          340          345          350
200 Pro Arg Thr His Glu Glu His Cys Gly
201          355          360

```

VERIFICATION SUMMARY

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Input Set : A:\LEX-0280-USA SEQLIST.txt

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date